

Resource Summary Report

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Mash

RRID:SCR_019135

Type: Tool

Proper Citation

Mash (RRID:SCR_019135)

Resource Information

URL: <https://github.com/marbl/Mash>

Proper Citation: Mash (RRID:SCR_019135)

Description: Software tool for genome and metagenome distance estimation using MinHash. Reduces large sequences and sequence sets to small, representative sketches, from which global mutation distances can be rapidly estimated.

Resource Type: software application, software resource, data analytics software

Defining Citation: [PMID:27323842](#)

Keywords: Genome distance estimation, metagenome distance estimation, MinHash, mutation distance, sequence, sequence set

Funding: NHGRI ;
NIH

Availability: Free, Available for download, Freely available

Resource Name: Mash

Resource ID: SCR_019135

Alternate IDs: OMICS_10468

Alternate URLs: <https://mash.readthedocs.io/en/latest/>,
<https://sources.debian.org/src/mash/>

License: BSD license

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260803T040757+0000

Ratings and Alerts

No rating or validation information has been found for Mash.

No alerts have been found for Mash.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 54 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

Kidenya BR, et al. (2025) Multidrug resistant hypervirulent ST307 clone from genomic surveillance of extended spectrum beta-lactamase-producing *Klebsiella pneumoniae* species complex in East Africa. *BMC microbiology*, 25(1), 755.

Azam S, et al. (2025) Advancing the Indian cattle pangenome: characterizing non-reference sequences in *Bos indicus*. *Journal of animal science and biotechnology*, 16(1), 21.

Xu Z, et al. (2025) PISAD: reference-free intraspecies sample anomalies detection tool based on k-mer counting. *GigaScience*, 14.

Shi H, et al. (2025) MAGs-based genomic comparison of gut significantly enriched microbes in obese individuals pre- and post-bariatric surgery across diverse locations. *Frontiers in cellular and infection microbiology*, 15, 1485048.

Guitor AK, et al. (2025) Megaplasmsids associate with *Escherichia coli* and other Enterobacteriaceae. *bioRxiv : the preprint server for biology*.

Tsui HT, et al. (2025) tRNA Modification Landscapes in Streptococci: Shared Losses and Clade-Specific Adaptations. *bioRxiv : the preprint server for biology*.

Kumari K, et al. (2025) In-depth genome and comparative genome analysis of a metal-resistant environmental isolate *Pseudomonas aeruginosa* S-8. *Frontiers in cellular and infection microbiology*, 15, 1511507.

Aguilar-Bultet L, et al. (2025) Genetic Cluster of Extended-Spectrum ??-lactamase-Producing *Klebsiella pneumoniae* in Humans and Food, Switzerland, 2018-2019. *Emerging infectious diseases*, 31(10), 2017.

Xu CCY, et al. (2025) Pre-exposure to stress reduces loss of community and genetic diversity following severe environmental disturbance. *Current biology : CB*, 35(5), 1061.

Hu Z, et al. (2024) Antimicrobial resistance survey and whole-genome analysis of nosocomial *P. Aeruginosa* isolated from eastern Province of China in 2016-2021. *Annals*

of clinical microbiology and antimicrobials, 23(1), 12.

Magne K, et al. (2024) Atypical rhizobia trigger nodulation and pathogenesis on the same legume hosts. *Nature communications*, 15(1), 9246.

Saunders M, et al. (2024) Outbreak of *Ralstonia pickettii* associated with contamination of saline products distributed internationally, the United Kingdom, 2024. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin*, 29(27).

Russo TA, et al. (2024) Differentiation of hypervirulent and classical *Klebsiella pneumoniae* with acquired drug resistance. *mBio*, 15(2), e0286723.

Weeber P, et al. (2024) A novel hybridization capture method for direct whole genome sequencing of clinical specimens to inform Legionnaires' disease investigations. *Journal of clinical microbiology*, 62(4), e0130523.

Foo A, et al. (2024) MosAIC: An annotated collection of mosquito-associated bacteria with high-quality genome assemblies. *PLoS biology*, 22(11), e3002897.

Williamson CHD, et al. (2024) ColiSeq: a multiplex amplicon assay that provides strain level resolution of *Escherichia coli* directly from clinical specimens. *Microbiology spectrum*, 12(6), e0413923.

Li H, et al. (2024) Protocol for isolating single species of bacteria with swarming ability from human feces. *STAR protocols*, 5(2), 102961.

Cook R, et al. (2024) Nanopore and Illumina sequencing reveal different viral populations from human gut samples. *Microbial genomics*, 10(4).

Thomas Iv JC, et al. (2024) Emergence and evolution of mosaic *penA-60* and *penA-237* alleles in a *Neisseria gonorrhoeae* core genogroup that was historically susceptible to extended spectrum cephalosporins. *Frontiers in microbiology*, 15, 1401303.

Johnson MC, et al. (2023) Core defense hotspots within *Pseudomonas aeruginosa* are a consistent and rich source of anti-phage defense systems. *Nucleic acids research*, 51(10), 4995.